



BOX SEQUENCE

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: C.L. Steele et al.

Attorney Docket No.: WSUR118414

Application No.: 10/025,145

Group Art Unit: 1638

Filed: December 19, 2001

Title: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)

RESPONSE TO THE NOTICE TO COMPLY WITH REQUIREMENTS FOR
PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE
AND/OR AMINO ACID SEQUENCE DISCLOSURE

Seattle, Washington 98101
June 27, 2002

TO THE COMMISSIONER FOR PATENTS:

Please enter the substitute sequence listing into the above-referenced patent application. Applicants note that SEQ ID NO:11 was erroneously identified as an artificial sequence in the original sequence listing. As set forth at page 31, lines 1-17, SEQ ID NO:11 discloses the sequence of a Grand Fir cDNA molecule. Thus, SEQ ID NO:11 is not an artificial sequence, and is not referred to as such in the substitute sequence listing.

Respectfully submitted,

CHRISTENSEN O'CONNOR
JOHNSON KINDNESS^{PLLC}

Barry F. McGurl
Registration No. 43,340
Direct Dial No. 206.695.1775

I hereby certify that this correspondence is being transmitted via FEDERAL EXPRESS addressed to the U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2001 South Clark Place, Arlington, VA 22202, on the below date.

Date:

6/27/02

BFM:jlj

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CHRISTENSEN O'CONNOR JOHNSON KINDNESS^{PLLC}
1420 Fifth Avenue
Suite 2800
Seattle, Washington 98101
206.682.8100



T.D

BOX SEQUENCE

OBICO Box 3

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

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Attorney Docket No.: WSUR118414

Application No.: 10/025,145

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Filed: December 19, 2001

Title: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)

TRANSMITTAL OF SUBSTITUTE SEQUENCE LISTING

Seattle, Washington 98101

June 27, 2002

TO THE COMMISSIONER FOR PATENTS:

A. Substitute Sequence Listing:

Transmitted herewith is a Response to the outstanding Formalities Letter, including the following:

1. Substitute sequence listing in computer readable form (diskette) and in paper copy form (83 pages), for entry into the above-identified application. The contents of the computer readable copy and paper copy of the substitute sequence listing are the same and contain no new matter.
2. Copy of the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosure
3. Copy of the Raw Sequence Listing Error Report.

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CHRISTENSEN O'CONNOR JOHNSON KINDNESS^{PLLC}
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Seattle, Washington 98101
206.682.8100



B. Additional Fee Charges or Credit for Overpayment

The Commissioner is hereby authorized to charge any fees under 37 C.F.R. §§ 1.16, 1.17 and 1.18 which may be required during the entire pendency of the application, or credit any overpayment, to Deposit Account No. 03-1740. This authorization also hereby includes a request for any extensions of time of the appropriate length required upon the filing of any reply during the entire prosecution of this application. A copy of this document is enclosed.

Respectfully submitted,

CHRISTENSEN O'CONNOR
JOHNSON KINDNESS^{PLLC}

Barry F. McGurl
Registration No. 43,340
Direct Dial No. 206.695.1775

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Date:

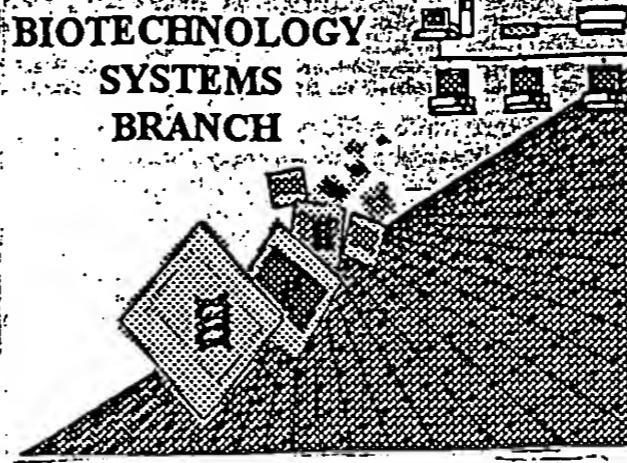
6/27/02

BFM:jlj

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0590

BIOTECHNOLOGY
SYSTEMS
BRANCH

0590

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/025,145
Source: OIPE
Date Processed by STIC: 1/15/2002

Anjum,
I couldn't find
disk

Anne.

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

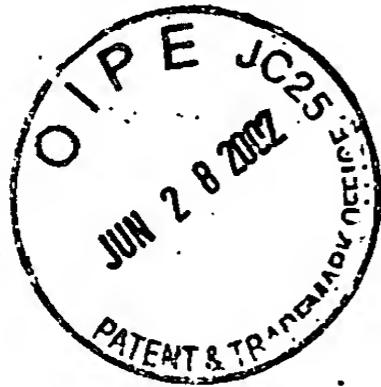
Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/025,145</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleics <input type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input checked="" type="checkbox"/> Use of <220>	Sequence(s) <u> </u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	



OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/025,145

DATE: 01/15/2002
TIME: 18:55:54

Input Set : A:\18414seq.txt
Output Set: N:\CRF3\01152002\J025145.raw

pp 6-7

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Croteau, Rodney B
 4 Bohlmann, Joerg
 5 Steele, Christopher L
 6 Phillips, Michael A
 8 <120> TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
 10 <130> FILE REFERENCE: WSUR18414
 12 <140> CURRENT APPLICATION NUMBER: US/10/025,145
 13 <141> CURRENT FILING DATE: 2001-12-19
 15 <150> PRIOR APPLICATION NUMBER: 09/360,545
 16 <151> PRIOR FILING DATE: 1999-07-26
 18 <150> PRIOR APPLICATION NUMBER: 60/052,249
 19 <151> PRIOR FILING DATE: 1997-07-11
 21 <150> PRIOR APPLICATION NUMBER: PCT/US98/14528
 22 <151> PRIOR FILING DATE: 1998-07-10
 24 <160> NUMBER OF SEQ ID NOS: 107
 26 <170> SOFTWARE: PatentIn Ver. 2.0
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 2196
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Abies grandis
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (69)..(1952)
 36 <223> OTHER INFORMATION: Clone AG2.2 encoding myrcene synthase
 38 <400> SEQUENCE: 1
 39 tgccggcacg aggttatctt gagtttcctc catataggcc aacacatatac atatcaaagg 60
 41 gagcaaga atg gct ctg gtt tct atc tca ccg ttg gct tcg aaa tct tgc 110
 42 Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys
 43. 1 5 10
 45 ctg cgc aag tcg ttg atc agt tca att cat gaa cat aag cct ccc tat 158
 46 Leu Arg Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr
 47 15 20 25 30
 49 aga aca atc cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg 206
 50 Arg Thr Ile Pro Asn Leu Gly Met Arg Arg Gly Lys Ser Val Thr
 51 35 40 45
 53 cct tcc atg agc atc agt ttg gcc acc gct gca cct gat gat ggt gta 254
 54 Pro Ser Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val
 55 50 55 60
 57 caa aga cgc ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc 302
 58 Gln Arg Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe
 59 65 70 75
 61 ata cag tct cta tca acg cct tat ggg gaa ccc tct tac cag gaa cgt 350
 62 Ile Gln Ser Leu Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Gln Glu Arg
 63 80 85 90
 65 gct gag aga tta att gtg gag gta aag aag ata ttc aat tca atg tac 398
 66 Ala Glu Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr
 67 95 100 105 110

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/025,145

DATE: 01/15/2002
TIME: 18:55:54

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Output Set: N:\CRF3\01152002\J025145.raw

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70	Leu	Asp	Asp	Gly	Arg	Leu	Met	Ser	Ser	Phe	Asn	Asp	Leu	Met	Gln	Arg	
71							115			120					125		
73	ctt	tgg	ata	gtc	gat	agc	gtt	gaa	cgt	ttg	ggg	ata	gct	aga	cat	ttc	494
74	Leu	Trp	Ile	Val	Asp	Ser	Val	Glu	Arg	Leu	Gly	Ile	Ala	Arg	His	Phe	
75							130			135					140		
77	aag	aac	gag	ata	aca	tca	gct	ctg	gat	tat	gtt	ttc	cgt	tac	tgg	gag	542
78	Lys	Asn	Glu	Ile	Thr	Ser	Ala	Leu	Asp	Tyr	Val	Phe	Arg	Tyr	Trp	Glu	
79							145			150					155		
81	gaa	aac	ggc	att	gga	tgt	ggg	aga	gac	agt	att	gtt	act	gtc	aac	590	
82	Glu	Asn	Gly	Ile	Gly	Cys	Gly	Arg	Asp	Ser	Ile	Val	Thr	Asp	Leu	Asn	
83							160			165					170		
85	tca	act	gcg	ttg	ggg	ttt	cga	act	ctt	cga	tta	cac	ggg	tac	act	gtt	638
86	Ser	Thr	Ala	Leu	Gly	Phe	Arg	Thr	Leu	Arg	Leu	His	Gly	Tyr	Thr	Val	
87	175						180			185					190		
89	tct	cca	gag	gtt	tta	aaa	gct	ttt	caa	gat	caa	aat	gga	cag	ttt	gta	686
90	Ser	Pro	Glu	Val	Leu	Lys	Ala	Phe	Gln	Asp	Gln	Asn	Gly	Gln	Phe	Val	
91							195			200					205		
93	tgc	tcc	ccc	ggt	cag	aca	gag	ggt	gag	atc	aga	agc	gtt	ctt	aac	tta	734
94	Cys	Ser	Pro	Gly	Gln	Thr	Glu	Gly	Glu	Ile	Arg	Ser	Val	Leu	Asn	Leu	
95							210			215					220		
97	tat	cgg	gct	tcc	ctc	att	gcc	ttc	cct	ggt	gag	aaa	gtt	atg	gaa	gaa	782
98	Tyr	Arg	Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu	Glu	
99							225			230					235		
101	gct	gaa	atc	ttc	tcc	aca	aga	tat	ttg	aaa	gaa	gct	cta	caa	aag	att	830
102	Ala	Glu	Ile	Phe	Ser	Thr	Arg	Tyr	Leu	Lys	Ala	Leu	Gln	Lys	Ile		
103	104	240					245						250				
105	cca	gtc	tcc	gct	ctt	tca	caa	gag	ata	aag	ttt	gtt	atg	gaa	tat	ggc	878
106	Pro	Val	Ser	Ala	Leu	Ser	Gln	Glu	Ile	Lys	Phe	Val	Met	Glu	Tyr	Gly	
107	255						260			265					270		
109	tgg	cac	aca	aat	ttg	cca	aga	ttg	gaa	gca	aga	aat	tac	ata	gac	aca	926
110	Trp	His	Thr	Asn	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Asp	Thr	
111							275			280					285		
113	ctt	gag	aaa	gac	acc	agt	gca	tgg	ctc	aat	aaa	aat	gct	ggg	aag	aag	974
114	Leu	Glu	Lys	Asp	Thr	Ser	Ala	Trp	Leu	Asn	Lys	Asn	Ala	Gly	Lys	Lys	
115							290			295					300		
117	ctt	tta	gaa	ctt	gca	aaa	ttg	gag	ttc	aat	ata	ttt	aac	tcc	tta	caa	1022
118	Leu	Leu	Glu	Leu	Ala	Lys	Leu	Glu	Phe	Asn	Ile	Phe	Asn	Ser	Leu	Gln	
119							305			310					315		
121	caa	aag	gaa	tta	caa	tat	ctt	ttg	aga	tgg	tgg	aaa	gag	tcg	gat	ttg	1070
122	Gln	Lys	Glu	Leu	Gln	Tyr	Leu	Leu	Arg	Trp	Trp	Lys	Glu	Ser	Asp	Leu	
123	320						325						330				
125	cct	aaa	ttg	aca	ttt	gct	cg	cat	cgt	cat	gtg	gaa	ttc	tac	act	ttg	1118
126	Pro	Lys	Leu	Thr	Phe	Ala	Arg	His	Arg	His	Val	Glu	Phe	Tyr	Thr	Leu	
127	335						340			345					350		
129	gcc	tct	tgt	att	gcc	att	gac	cca	aaa	cat	tct	gca	ttc	aga	cta	ggc	1166
130	Ala	Ser	Cys	Ile	Ala	Ile	Asp	Pro	Lys	His	Ser	Ala	Phe	Arg	Leu	Gly	
131							355			360					365		
133	ttc	gcc	aaa	atg	tgt	cat	ctt	gtc	aca	gtt	ttg	gac	gat	att	tac	gac	1214

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/025,145

DATE: 01/15/2002
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Input Set : A:\18414seq.txt
Output Set: N:\CRF3\01152002\J025145.raw

134	Phe	Ala	Lys	Met	Cys	His	Leu	Val	Thr	Val	Leu	Asp	Asp	Ile	Tyr	Asp	
135				370					375					380			
137	act	ttt	gga	acg	att	gac	gag	ctt	gaa	ctc	tcc	aca	tct	gca	att	aag	1262
138	Thr	Phe	Gly	Thr	Ile	Asp	Glu	Leu	Glu	Leu	Phe	Thr	Ser	Ala	Ile	Lys	
139					385				390					395			
141	aga	tgg	aat	tca	tca	gag	ata	gaa	cac	ctt	cca	gaa	tat	atg	aaa	tgt	1310
142	Arg	Trp	Asn	Ser	Ser	Glu	Ile	Glu	His	Leu	Pro	Glu	Tyr	Met	Lys	Cys	
143					400				405					410			
145	gtg	tac	atg	gtc	gtg	ttt	gaa	act	gta	aat	gaa	ctg	aca	cga	gag	gcg	1358
146	Val	Tyr	Met	Val	Val	Phe	Glu	Thr	Val	Asn	Glu	Leu	Thr	Arg	Glu	Ala	
147	415					420				425				430			
149	gag	aag	act	caa	ggg	aga	aac	act	ctc	aac	tat	gtt	cga	aag	gct	tgg	1406
150	Glu	Lys	Thr	Gln	Gly	Arg	Asn	Thr	Leu	Asn	Tyr	Val	Arg	Lys	Ala	Trp	
151						435				440				445			
153	gag	gct	tat	ttt	gat	tca	tat	atg	gaa	gaa	gca	aaa	tgg	atc	tct	aat	1454
154	Glu	Ala	Tyr	Phe	Asp	Ser	Tyr	Met	Glu	Glu	Ala	Lys	Trp	Ile	Ser	Asn	
155						450			455				460				
157	ggt	tat	ctg	cca	atg	ttt	gaa	gag	tac	cat	gag	aat	ggg	aaa	gtg	agc	1502
158	Gly	Tyr	Leu	Pro	Met	Phe	Glu	Glu	Tyr	His	Glu	Asn	Gly	Lys	Val	Ser	
159						465			470				475				
161	tct	gca	tat	cgc	gta	gca	aca	ttg	caa	ccc	atc	ctc	act	ttg	aat	gca	1550
162	Ser	Ala	Tyr	Arg	Val	Ala	Thr	Leu	Gln	Pro	Ile	Leu	Thr	Leu	Asn	Ala	
163						480			485				490				
165	tgg	ctt	cct	gat	tac	atc	ttg	aag	gga	att	gat	ttt	cca	tcc	agg	ttc	1598
166	Trp	Leu	Pro	Asp	Tyr	Ile	Leu	Lys	Gly	Ile	Asp	Phe	Pro	Ser	Arg	Phe	
167	495						500			505				510			
169	aat	gat	ttg	gca	tcg	tcc	ttc	ctt	cg	cta	cga	ggt	gac	aca	cgc	tgc	1646
170	Asn	Asp	Leu	Ala	Ser	Ser	Phe	Leu	Arg	Leu	Arg	Gly	Asp	Thr	Arg	Cys	
171						515				520				525			
173	tac	aag	gcc	gat	agg	gat	cgt	ggt	gaa	gaa	gct	tcg	tgt	ata	tca	tgt	1694
174	Tyr	Lys	Ala	Asp	Arg	Asp	Arg	Gly	Glu	Glu	Ala	Ser	Cys	Ile	Ser	Cys	
175						530			535				540				
177	tat	atg	aaa	gac	aat	cct	gga	tca	acc	gaa	gaa	gat	gcc	ctc	aat	cat	1742
178	Tyr	Met	Lys	Asp	Asn	Pro	Gly	Ser	Thr	Glu	Glu	Asp	Ala	Leu	Asn	His	
179						545			550				555				
181	atc	aat	gcc	atg	gtc	aat	gac	ata	atc	aaa	gaa	tta	aat	tgg	gaa	ctt	1790
182	Ile	Asn	Ala	Met	Val	Asn	Asp	Ile	Ile	Lys	Glu	Leu	Asn	Trp	Glu	Leu	
183						560			565				570				
185	cta	aga	tcc	aac	gac	aat	att	cca	atg	ctg	gcc	aag	aaa	cat	gct	ttt	1838
186	Leu	Arg	Ser	Asn	Asp	Asn	Ile	Pro	Met	Leu	Ala	Lys	Lys	His	Ala	Phe	
187	575						580			585				590			
189	gac	ata	aca	aga	gct	ctc	cac	cat	ctc	tac	ata	tat	cga	gat	ggc	ttt	1886
190	Asp	Ile	Thr	Arg	Ala	Leu	His	His	Leu	Tyr	Ile	Tyr	Arg	Asp	Gly	Phe	
191						595				600				605			
193	agt	gtt	gcc	aac	aag	aca	aaa	aaa	ttg	gtt	atg	gaa	aca	ctc	ctt		1934
194	Ser	Val	Ala	Asn	Lys	Glu	Thr	Lys	Lys	Leu	Val	Met	Glu	Thr	Leu	Leu	
195						610			615				620				
197	gaa	tct	atg	ctt	ttt	taa	ctataaccat	atccataata	ataagctcat								1982
198	Glu	Ser	Met	Leu	Phe												

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/025,145

DATE: 01/15/2002
TIME: 18:55:54

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 201 aatgctaaat tattggcctt atgacatagt ttatgtatgt acttgtgtga attcaatcat 2042.
 203 atcggtgtgg tatgattaaa aagctagagc ttacttagtt agtaacatgg tgataaaaagt 2102
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 212 <212> TYPE: PRT
 213 <213> ORGANISM: Abies grandis
 215 <400> SEQUENCE: 2
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 217 1 5 10 15
 219 Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr
 220 20 25 30
 222 Ile Pro Asn Leu Gly Met Arg Arg Gly Lys Ser Val Thr Pro Ser
 223 35 40 45
 225 Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg
 226 50 55 60
 228 Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln
 229 65 70 75 80
 231 Ser Leu Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu
 232 85 90 95
 234 Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp
 235 100 105 110
 237 Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp
 238 115 120 125
 240 Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn
 241 130 135 140
 243 Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn
 244 145 150 155 160
 246 Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr
 247 165 170 175
 249 Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro
 250 180 185 190
 252 Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser
 253 195 200 205
 255 Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg
 256 210 215 220
 258 Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu
 259 225 230 235 240
 261 Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val
 262 245 250 255
 264 Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly Trp His
 265 260 265 270
 267 Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr Leu Glu
 268 275 280 285
 270 Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys Leu Leu
 271 290 295 300
 273 Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln Gln Lys

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/025,145

DATE: 01/15/2002
TIME: 18:55:54

Input Set : A:\18414seq.txt
Output Set: N:\CRF3\01152002\J025145.raw

274	305	310	315	320
276	Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu Pro Lys			
277	325	330	335	
279	Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser			
280	340	345	350	
282	Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala			
283	355	360	365	
285	Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe			
286	370	375	380	
288	Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp			
289	385	390	395	400
291	Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr			
292	405	410	415	
294	Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala Glu Lys			
295	420	425	430	
297	Thr Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala			
298	435	440	445	
300	Tyr Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr			
301	450	455	460	
303	Leu Pro Met Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala			
304	465	470	475	480
306	Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu			
307	485	490	495	
309	Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp			
310	500	505	510	
312	Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys			
313	515	520	525	
315	Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met			
316	530	535	540	
318	Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn			
319	545	550	555	560
321	Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg			
322	565	570	575	
324	Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile			
325	580	585	590	
327	Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val			
328	595	600	605	
330	Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu Glu Ser			
331	610	615	620	
333	Met Leu Phe			
334	625			
337	<210> SEQ ID NO: 3			
338	<211> LENGTH: 2018			
339	<212> TYPE: DNA			
340	<213> ORGANISM: Abies grandis			
342	<220> FEATURE:			
343	<221> NAME/KEY: CDS			
344	<222> LOCATION: (6)..(1892)			
345	<223> OTHER INFORMATION: Clone AG3.18 encoding pinene synthase			

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6

<210> 11
<211> 108
<212> DNA
<213>
<220>
<223>
<400> 11

gatgatgggt ttgatgcgca cggaacccta gatgaattga agctattcac tgaggctgtg 60
agaagatggg acctctcctt tacagacaac ttcccccatt acatgaaa 108

Artificial Sequence

see item 11 on Exam Summary Sheet

PMS

The use of n or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
definition is presented in the <220> to <223> fields of
each sequence using n or Xaa.

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<210> 25

<211> 8

<212> PRT

<213> : Artificial Sequence

<220>

<223>

Description of Artificial Sequence: conserved

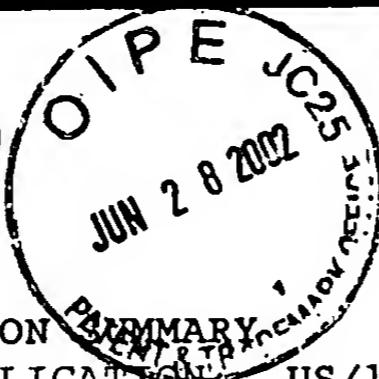
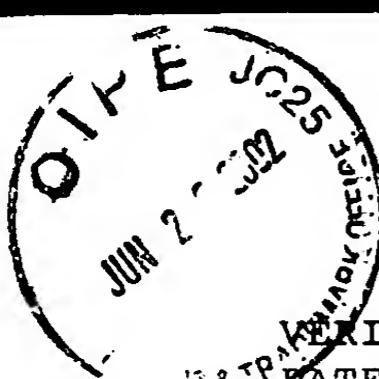
amino acid motif on which the sequence of Primer D
was based, wherein Xaa at position number 3 represents Thr or Ile, Xaa at
position number 4 represents Ile or Tyr or Phe, Xaa at position number 6

L2207 ← L2237 represents Ala or Val and Xaa at position number 8 represents Ala or Gly

Per 1.823 of Sequence Rules, 4 lines maximum
for L2237 response. Insert another L2207 after
4th line and insert a L2237 on 5th line.

IMPORTANT:

The types of errors shown exist throughout
the entire listing. Please check subsequent
sequences for similar errors.



VERIFICATION SUMMARY
PATENT APPLICATION US/10/025,145

DATE: 01/15/2002
TIME: 18:55:55

Input Set : A:\18414seq.txt
Output Set: N:\CRF3\01152002\J025145.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:963 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:983 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1003 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1023 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1031 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1031 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1061 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1077 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1949 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1969 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1989 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:2027 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2036 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:2058 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:2072 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2081 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:2102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:2609 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:45
L:2609 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:45
L:2609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:2623 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2626 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
L:2626 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
L:2626 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:2672 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2689 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2692 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:50
L:2692 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:50
L:2692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:2706 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2709 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:51
L:2709 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:51
L:2709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:2723 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2726 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:52
L:2726 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:52
L:2726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:2740 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2743 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:53
L:2743 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:53
L:2743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:2786 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:56
L:2786 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:56
L:2786 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56